

WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a member selected from the group consisting of:

5 (a) a polynucleotide having at least 75% sequence identity, as determined by the GAP algorithm under default parameters, to a polynucleotide of SEQ ID NO: 1;

(b) a polynucleotide encoding a polypeptide of SEQ ID NO: 2;

(c) a polynucleotide amplified from a nucleic acid library using primers which 10 selectively hybridize, under stringent hybridization conditions, to loci within a polynucleotide of SEQ ID NO: 1;

(d) a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 0.1X SSC at about 60 to 65°C, to a polynucleotide of SEQ ID NO: 1;

(e) a polynucleotide of SEQ ID NO: 1;

(f) a polynucleotide which is complementary to a polynucleotide of (a), (b), (c), or (e); and

(g) a polynucleotide comprising at least 50 contiguous nucleotides from a 15 polynucleotide of (a), (b), (c), (d), (e), or (f).

2. A recombinant expression cassette, comprising a member of claim 1 operably linked, in sense or anti-sense orientation, to a promoter.

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3. A host cell comprising the recombinant expression cassette of claim 2.

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4. A transgenic plant comprising a recombinant expression cassette of claim 2.

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5. The transgenic plant of claim 4, wherein said plant is a monocot.

6. The transgenic plant of claim 4, wherein said plant is selected from the group consisting of: maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, and millet.

5 7. A transgenic seed from the transgenic plant of claim 4.

8. A method of modulating the level of nitrate-responsive root transcriptional factor in a plant, comprising:

10 (a) introducing into a plant cell a recombinant expression cassette comprising a root transcriptional factor polynucleotide of claim 1 operably linked to a promoter;

15 (b) culturing the plant cell under plant cell growing conditions;

(c) regenerating a plant from said plant cell; and

(d) inducing expression of said polynucleotide for a time sufficient to modulate the level of nitrate-responsive root transcriptional factor in said plant.

9. The method of claim 8, wherein the plant is maize.

10. An isolated protein comprising a member selected from the group 20 consisting of:

25 (a) a polypeptide of at least 20 contiguous amino acids from a polypeptide of SEQ ID NO: 2;

(b) a polypeptide of SEQ ID NO: 2;

(c) a polypeptide having at least 75% sequence identity to, and having at least one epitope in common with, a polypeptide of SEQ ID NO: 2, wherein said sequence identity is determined by the GAP algorithm under default parameters; and,

(d) at least one polypeptide encoded by a member of claim 1.